

## Appendix A



## Blast 2 Sequences results

PubMed

Entrez

BLAST

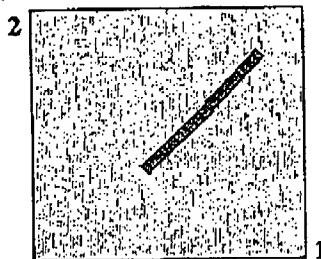
OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.10 [Oct-19-2004]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ Align ☐

Sequence 1 **lcl|seq\_1** Length 1132 (1 .. 1132)Sequence 2 **lcl|seq\_2** Length 3279 (1 .. 3279)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 153 bits (387), Expect = 2e-34  
Identities = 118/507 (23%), Positives = 220/507 (43%), Gaps = 30/507 (5%)  
Frame = +2

```
Query: 464 FVRACLRRLVPPGLWGSRHNERFLRNTKFFISLGKHA KLSLQELTWKMSVRDCAWLRRS 523
          F+ ++P R N + F + KK++ L KH + L K++ R+ +W++
Sbjct: 1181 FINEFFYNILPKDFLTGR-NRKNFQKKVKYVELNKH E L I H K N L L L E K I N T R E I S W M Q V E 1357

Query: 524 PGVGCVPAAEHRRLREEILAKFLHWLMSVYVELLRSEFFYVTETTFQKNRLFFYRKSVWSK 583
          +H +L K L W+ VV L+R FFYVTE ++ ++YRK++W
Sbjct: 1358 TSAKHFFYFDHE-NIYVLWKLRLRWIFEDLVVSLIR*FFYVTEQQKSYSKTYYYRKNIWDV 1534

Query: 584 LQSIGIRQHLKRVQLRELSEAEVRQHREARFALLTSRLRFIPKPDGLRPVNM DYVVGAR 643
          + + I LK+ L E+ E EV + +++ +LR IPK RPI+ + +
Sbjct: 1535 IMKMSIAD-LKKETLAEVQEKEVEEWKKS L-GFAPGKLR LIPKKTTFRPIMTFN----KK 1696

Query: 644 TFRREKRAERLTSRVKALFSVLNYERARR---PGLLGASVLGLDDI HRAWRTFVLRVRAQ 700
          +++ +LT+ K L S L + + G +V DD+ + + EV + + Q
Sbjct: 1697 IVNSDRKTTKLTNTKLLNSHMLKTLK NRMFKDFFGFAVENYDDVMKKYEEFVCKWK-Q 1873

Query: 701 DPPPPELYFVKVDVTGAYDTIPQDRLTEVI-----ASIIKPQNTYCVRRYAV 746
          F+L+F +D+ YD++ +++L+ + A I+K +N +
Sbjct: 1874 VGQPKLFFATMDIEK*YDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVIDS KNF 2053

Query: 747 VQKAAGHGVRAKFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAV VIEQSSSLNEASSGLF 806
          +K + R+ F+ ++ P + + + Q + +++E L
Sbjct: 2054 RKKEMKDYFRQKFQK-IALEGGQYPTLFSVLENEQNDLNAKKT LIVEAKQRNYFKKDNLL 2230

Query: 807 DVFLRFMCHHAVRIRCKSYVQCQGI PQCSILSTLLCSLCYGD MENKLEFAGIRRD----- 860
```

+ ++ + GK Y Q +GIPQG +S++L S Y +E +R +  
 Sbjct: 2231 QPVINICQYNYINFNGKEYKQTKGIPQGL\*VSSILSSFYATLEESSLGFLRDESMNPEN 2410  
 Query: 861 ---GLLRLRVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNLAKTVVNFVPEDEALGGT 917  
 LL+RL DD+LL+T +A F+ L+ E G N++K +FP+  
 Sbjct: 2411 PNVNLLMRLTDDYLLITTQENNAVLFIKELINVSRENGFKTNMKKLQTSFPLSPSKEAKY 2590  
 Query: 918 AFVQMPAHGLF----PWCGLLLDTRTL 940  
 + + W G+ +D +TL  
 Sbjct: 2591 GMDSVEEQNIVQDYCDWIGISIDMKTL 2671

CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total secs.

Lambda K H  
 0.324 0.138 0.434

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Sequences: 1  
 Number of Hits to DB: 33,746  
 Number of extensions: 24580  
 Number of successful extensions: 7  
 Number of sequences better than 10.0: 1  
 Number of HSP's better than 10.0 without gapping: 1  
 Number of HSP's gapped: 2  
 Number of HSP's successfully gapped: 1  
 Number of extra gapped extensions for HSPs above 10.0: 0  
 Length of query: 1132  
 Length of database: 4,092,316,854  
 Length adjustment: 153  
 Effective length of query: 979  
 Effective length of database: 4,092,316,701  
 Effective search space: 4006378050279  
 Effective search space used: 4006378050279  
 Neighboring words threshold: 9  
 Window for multiple hits: 0  
 X1: 15 ( 7.0 bits)  
 X2: 129 (49.7 bits)  
 X3: 129 (49.7 bits)  
 S1: 40 (21.6 bits)  
 S2: 46 (22.3 bits)

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*Facsimile Transmittal Sheet*

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